



FIG. 1A

5' 11 20 29 38 47 56
 GAG ACT CAC GGT CAA GCT AAG GCG AAG AGT GGG TGG CTG AAG CCA TAC TAT TTT

 65 74 83 92 101 110
 ATA GAA TTA ATG GAA AGC AGA AAA GAC ATC ACA AAC CAA GAA GAA CTT TGG AAA

 M E S R K D I T N Q E E L W K

 119 128 137 146 155 164
 ATG AAG CCT AGG AGA AAT TTA GAA GAA GAC GAT TAT TTG CAT AAG GAC ACG GGA

 M K P R R N L E E D D Y L H K D T G

 173 182 191 200 209 218
 GAG ACC AGC ATG CTA AAA AGA CCT GTG CTT TTG CAT TTG CAC CAA ACA GCC CAT

 E T S M L K R P V L L H L H Q T A H

 227 236 245 254 263 272
 GCT GAT GAA TTT GAC TGC CCT TCA GAA CTT CAG CAC ACA CAG GAA CTC TTT CCA

 A D E F D C P S E L Q H T Q E L F P

 281 290 299 308 317 326
 CAG TGG CAC TTG CCA ATT AAA ATA GCT GCT ATT ATA GCA TCT CTG ACT TTT CTT

 Q W H L P I K I A A I I A S L T F L

 335 344 353 362 371 380
 TAC ACT CTT CTG AGG GAA GTA ATT CAC CCT TTA GCA ACT TCC CAT CAA CAA TAT

 Y T L L R E V I H P L A T S H Q Q Y

 389 398 407 416 425 434
 TTT TAT AAA ATT CCA ATC CTG GTC ATC AAC AAA GTC TTG CCA ATG GTT TCC ATC

 F Y K I P I L V I N K V L P M V S I

 443 452 461 470 479 488
 ACT CTC TTG GCA TTG GTT TAC CTG CCA GGT GTG ATA GCA GCA ATT GTC CAA CTT

 T L L A L V Y L P G V I A A I V Q L

 497 506 515 524 533 542
 CAT AAT GGA ACC AAG TAT AAG AAG TTT CCA CAT TGG TTG GAT AAG TGG ATG TTA

 H N G T K Y K K F P H W L D K W M L

 551 560 569 578 587 596
 ACA AGA AAG CAG TTT GGG CTT CTC AGT TTC TTT TTT GCT GTA CTG CAT GCA ATT

 T R K Q F G L L S F F F A V L H A I

 605 614 623 632 641 650
 TAT AGT CTG TCT TAC CCA ATG AGG CGA TCC TAC AGA TAC AAG TTG CTA AAC TGG

 Y S L S Y P M R R S Y R Y K L L N W

REPLACEMENT SHEET

659	668	677	686	695	704
GCA TAT CAA CAG GTC	CAA CAA AAT AAA	GAA GAT GCC TGG	ATT GAG CAT GAT	GTT	

A Y Q Q V Q Q N K E D A W I E H D V					
713	722	731	740	749	758
TGG AGA ATG GAG ATT	TAT GTG TCT CTG	GGA ATT GTG	GGA TTG GCA	ATA CTG	GCT

W R M E I Y V S L G I V G L A I L A					
767	776	785	794	803	812
CTG TTG GCT GTG ACA	TCT ATT CCA TCT	GTG AGT GAC TCT	TTG ACA TGG	AGA GAA	

L L A V T S I P S V S D S L T W R E					
821	830	839	848	857	866
TTT CAC TAT ATT CAG	AGC AAG CTA GGA	ATT GTT TCC CTT	CTA CTG GGC	ACA ATA	

F H Y I Q S K L G I V S L L L G T I					
875	884	893	902	911	920
CAC GCA TTG ATT TTT	GCC TGG AAT AAG	TGG ATA GAT ATA	AAA CAA TTT	GTA TGG	

H A L I F A W N K W I D I K Q F V W					
929	938	947	956	965	974
TAT ACA CCT CCA ACT	TTT ATG ATA GCT	GTT TTC CTT CCA	ATT GTT GTC	CTG ATA	

Y T P P T F M I A V F L P I V V L I					
983	992	1001	1010	1019	1028
TTT AAA AGC ATA CTA	TTC CTG CCA TGC	TTG AGG AAG AAG	ATA CTG AAG	ATT AGA	

F K S I L F L P C L R K K I L K I R					
1037	1046	1055	1064	1073	1082
CAT GGT TGG GAA GAC	GTC ACC AAA ATT	AAC AAA ACT GAG	ATA TGT TCC	CAG TTG	

H G W E D V T K I N K T E I C S Q L					
1091	1100	1109	1118	1127	1136
TAG AAT TAC TGT TTA	CAC ACA TTT TTG	TTC AAT ATT GAT	ATA TTT TAT	CAC CAA	

* N Y C L H T F L F N I D I F Y H Q					
1145	1154	1163	1172	1181	1190
CAT TTC AAG TTT GTA	TTT GTT AAT AAA	ATG ATT ATT CAA	GGA AAA AAA	AAA AAA	

H F K F V F V N K M I I Q G K K K K					

AAA AA 3' SEQ ID NO:1

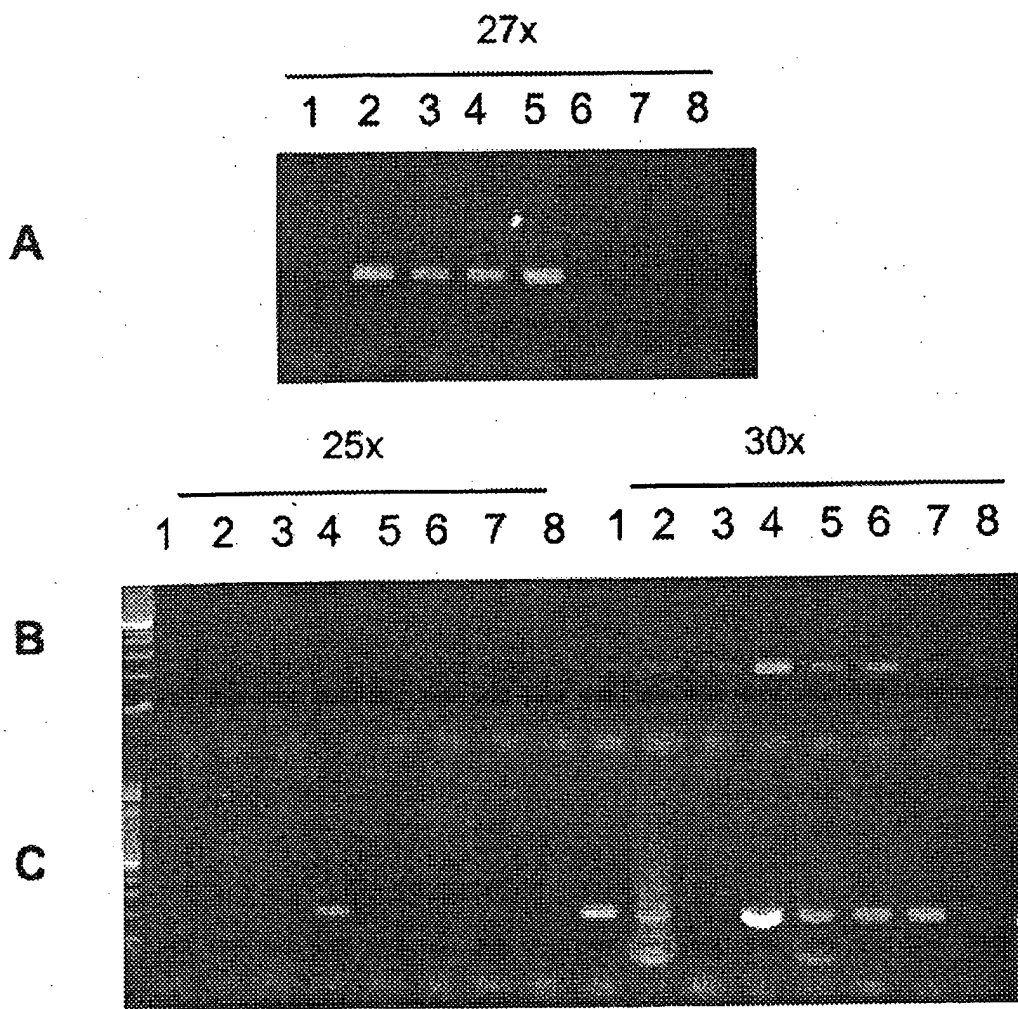
K

SEQ ID NO:2

FIG. 1C

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG
GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT
AAC AGC AAG 3' SEQ ID NO:3

FIG. 2



Panels:

A

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

B

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

C

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG. 4

GGGGCCCGCACCTCTGGGCAGCAGCGGCAGCCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCC
ATACTATTTTATAGAATTAATGGAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG
AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC
ATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCACA
GTGGCACTTGCCAATTAATAAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATT
CACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGG
TTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACCTCATAATGGAACCA
GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTT
GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAT
ATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCT
GGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGG
AGAGAATTTCACTATATTCAGGTAAATAATATATAAAATAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGAT
ATAGAATATGTTGACTTTACCCCATAAAAATAACAAATGTTTTCAACAGCAAAGATCTTATACTTGTTCOAATT
AATAATGTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTCCTAGACATAAATAAAGGCAT
TAAATATTCTTTGTTTTTTTTTTTTGTTTGTGTTGTTTTGTTTGTGTTGTTTGTGTTTGTGTTTGTGATGAAGTCTCG
CTCTGTTGCCCATGCTGGAGTACAGTGGCAGCATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTCCAGGCGATT
TCTTGCCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTAGTA
GAGACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCCCACCTCGGCCTCCC
AAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCTGCTCTTTCTAATATTTGAAACTTGTTAGACAATTT
GCTACCCATCTAATGTGATATTTAGGAATCCAATATGCATGGTTTATTATTTCTTAAAAAAATATTCTTTTACC
TGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACCTTAGCACTTCCAGAAACAAAACTCTCTCCTTGAAA
TAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTTATAT
ACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAACTATCTCAGATTTACTGAGGTTTATCTTCTGGT
GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGTCTGACAAGATTCAAAGGACTAAA
TTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCAGACATT
CGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGGAAAGTATGC
CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAAATTCCTAATTTTGTAGGTTTCTAG
CCTGATAACCACTGGAGTTCTTTGGTCCTCATTAAATAGCTTTCTTACACATTGCTCTGCCTGTTACACATATGA
TGAACACTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACCTGAGCCTATTCTACTATATGTACA

ATACCTAGCCCATAAAGGTATACAATACACATTTGGTAAACTAATTTTCAACCAATGACATGTATTTTCAACT
AGTAACCTAGAAATGTTTCACTTAAATCTGAGAAGTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAA
ACGCAAACCTAGCTATTTGATTGTATTCACTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTTCGATTTGTTCT
GGCAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTCAGAACACCGT
TGAGATTACATAGGTGAACAACTATTTTAAAGCAACTTTATTTGTGTAGTGACAAAGCATCCCAATGCAGGCTGAA
ATGTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATTGTTTCATATTATTTCCATGTTATC
AGAATATTTGATTTTTTAAAAACATAGGCCAAGTTCATTCACTTCATTATTTCATTATCAAAATCAGAGTGAATCA
CATTAGTCGCCTTCACAACTGATAAAGATCACTGAAGTCAAATTGATTTTTGCTATAATCTTCAATCTACCTATAT
TTAATTGAGAATCTAAATGTACAAATCATTGTGTTGATTCTGCAGTGATCCTGTATAAGTAAGACTCAGTCCCT
GATTTTAGGTATCCTGTGAAAAGCAGAATTAAGACAAATACACAAGAGACAAAGCACAAAAATAAATATCATAAG
GGGATGAACAAAATGGTGGAGAAAGAGTAGACAAAGTTTTTGATCACCTGCCTTCAAAGAAAGGCTGTGAATTTTG
TTCACCTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAAGAGCAGAAAGATG
TGAATGGACATTGTTGAGAAATGTGATAGGAAAACAATCATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAG
ATGAGGTAGGATGGGATAAACTCTTATTGAACCAATCTTCACCAATTTTGTTTTCTTTTGAGAGCAAGCTAGGA
ATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTG
TATGGTATACACCTCCAACCTTTTATGATAGCTGTTTTCTTCCAATTGTTGTCCTGATATTTAAAAGCATACTATT
CCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACCTGAG
ATATGTTCCAGTTGTAGAAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCACATTTC
AGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAAA SEQ ID NO:6

FIG. 5

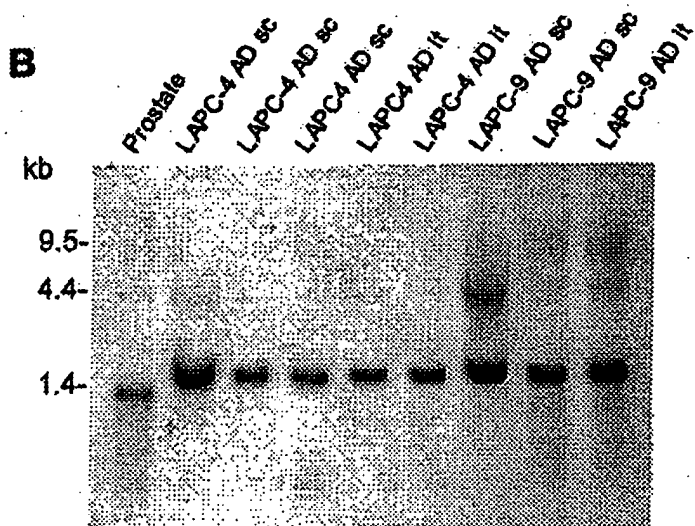
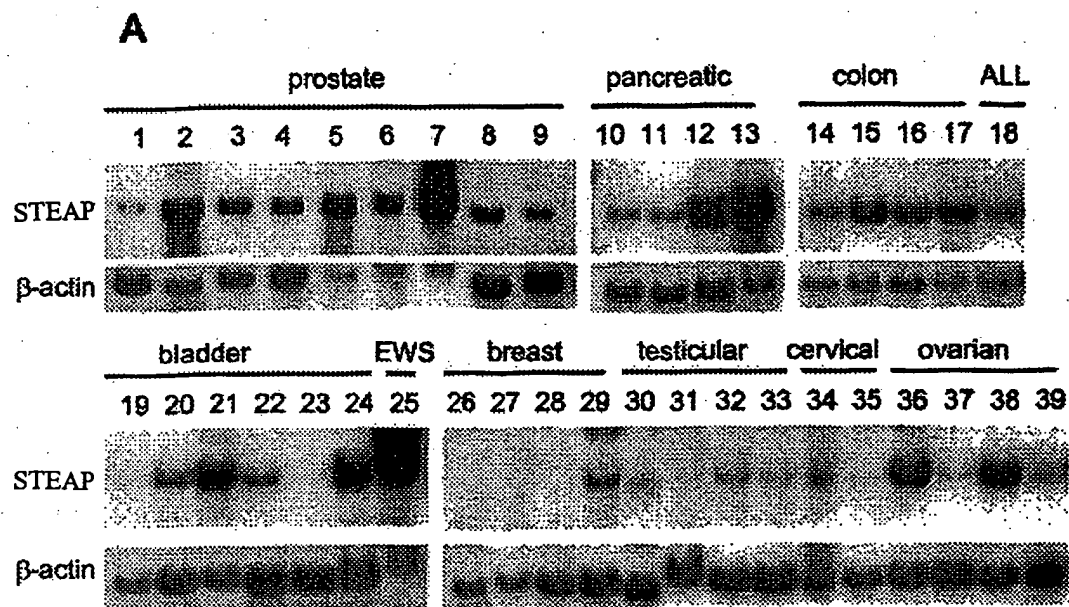


FIG. 6

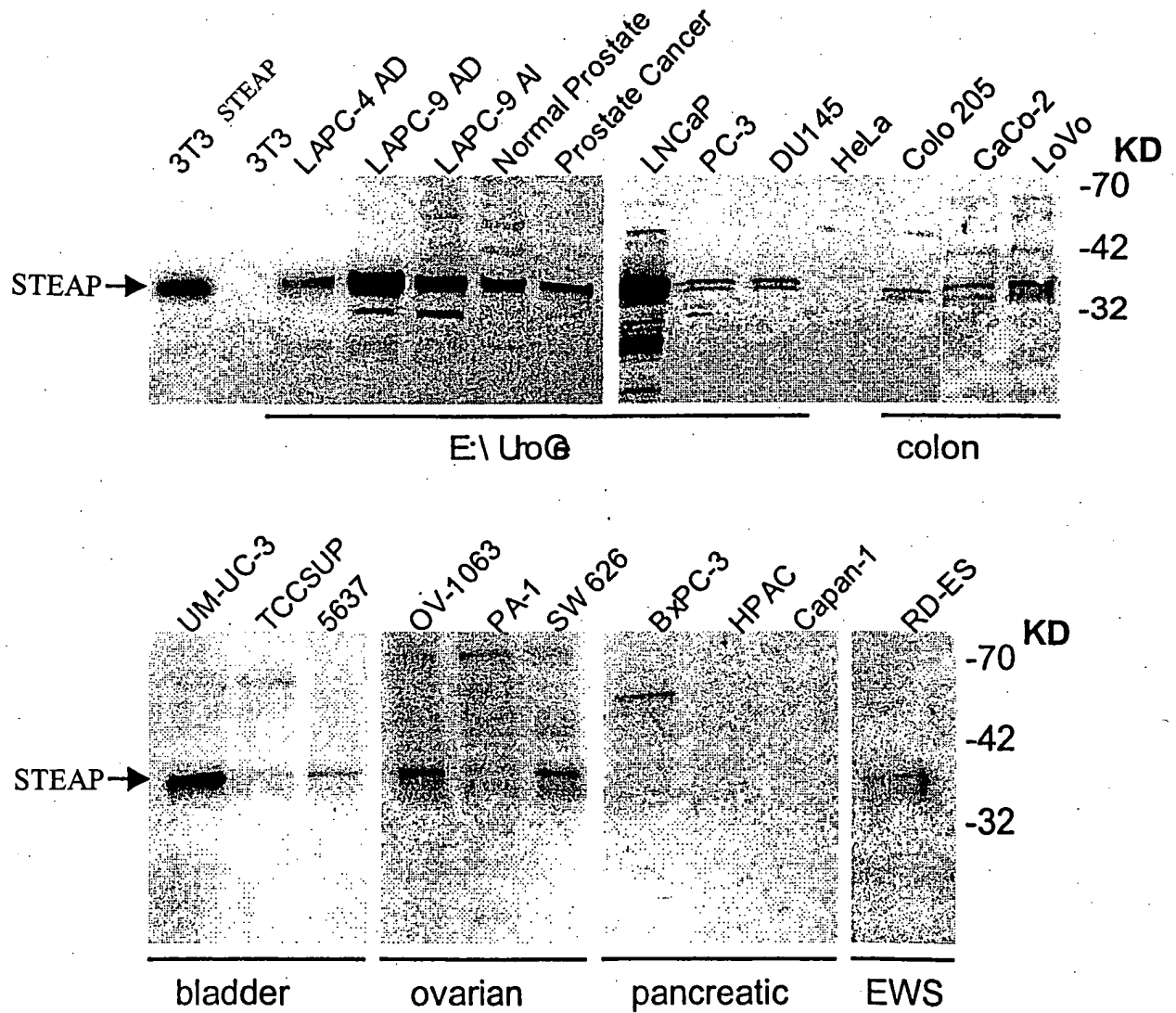
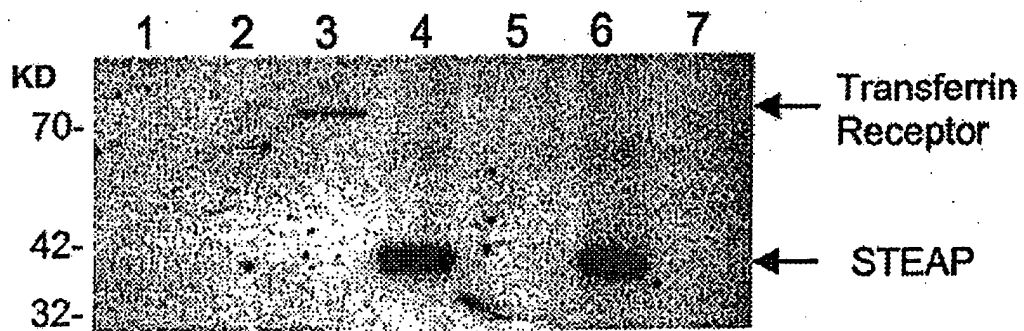


FIG. 7

A



B

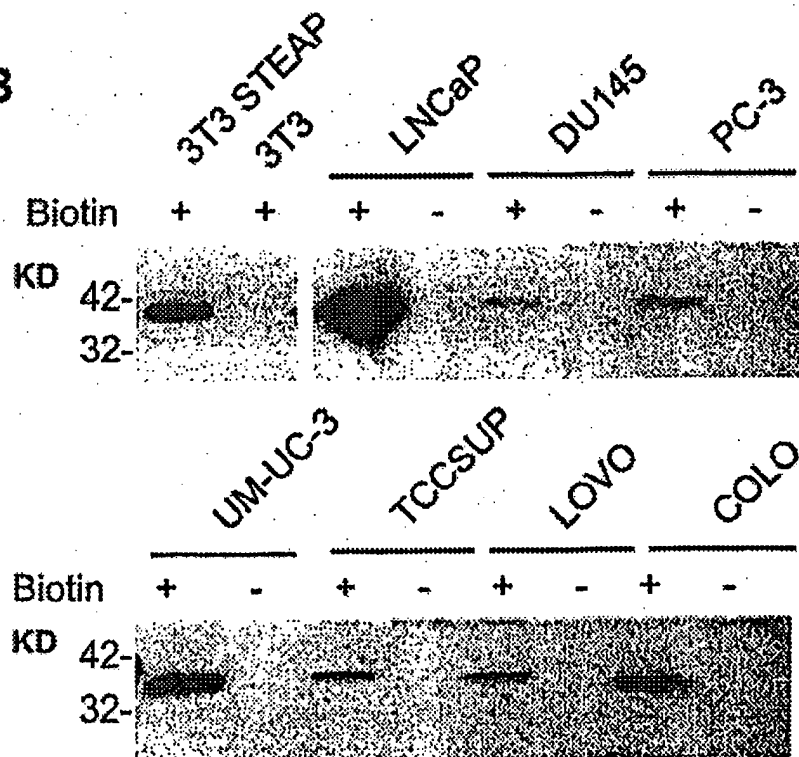


FIG. 9

	10			19			28			37			46			55		
5'	GAC	TTT	TAC	AAA	ATT	CCT	ATA	GAG	ATT	GTG	AAT	AAA	ACC	TTA	CCT	ATA	GTT	GCC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Asp	Phe	Tyr	Lys	Ile	Pro	Ile	Glu	Ile	Val	Asn	Lys	Thr	Leu	Pro	Ile	Val	Ala
		64			73			82			91			100				109
	ATT	ACT	TTG	CTC	TCC	CTA	GTA	TAC	CTC	GCA	GGT	CTT	CTG	GCA	GCT	GCT	TAT	CAA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ile	Thr	Leu	Leu	Ser	Leu	Val	Tyr	Leu	Ala	Gly	Leu	Leu	Ala	Ala	Ala	Tyr	Gln
		118			127			136			145			154				163
	CTT	TAT	TAC	GGC	ACC	AAG	TAT	AGG	AGA	TTT	CCA	CCT	TGG	TTG	GAA	ACC	TGG	TTA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Tyr	Tyr	Gly	Thr	Lys	Tyr	Arg	Arg	Phe	Pro	Pro	Trp	Leu	Glu	Thr	Trp	Leu
		172			181			190			199			208				217
	CAG	TGT	AGA	AAA	CAG	CTT	GGA	TTA	CTA	AGT	TTT	TTC	TTC	GCT	ATG	GTC	CAT	GTT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Gln	Cys	Arg	Lys	Gln	Leu	Gly	Leu	Leu	Ser	Phe	Phe	Phe	Ala	Met	Val	His	Val
		226			235			244			253			262				271
	GCC	TAC	AGC	CTC	TGC	TTA	CCG	ATG	AGA	AGG	TCA	GAG	AGA	TAT	TTG	TTT	CTC	AAC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ala	Tyr	Ser	Leu	Cys	Leu	Pro	Met	Arg	Arg	Ser	Glu	Arg	Tyr	Leu	Phe	Leu	Asn
		280			289			298			307			316				325
	ATG	GCT	TAT	CAG	CAG	GTT	CAT	GCA	AAT	ATT	GAA	AAC	TCT	TGG	AAT	GAG	GAA	GAA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Met	Ala	Tyr	Gln	Gln	Val	His	Ala	Asn	Ile	Glu	Asn	Ser	Trp	Asn	Glu	Glu	Glu
		334			343			352			361			370				379
	GTT	TGG	AGA	ATT	GAA	ATG	TAT	ATC	TCC	TTT	GGC	ATA	ATG	AGC	CTT	GGC	TTA	CTT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Val	Trp	Arg	Ile	Glu	Met	Tyr	Ile	Ser	Phe	Gly	Ile	Met	Ser	Leu	Gly	Leu	Leu
		388			397			406			415			424				433
	TCC	CTC	CTG	GCA	GTC	ACT	TCT	ATC	CCT	TCA	GTG	AGC	AAT	GCT	TTA	AAC	TGG	AGA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ser	Leu	Leu	Ala	Val	Thr	Ser	Ile	Pro	Ser	Val	Ser	Asn	Ala	Leu	Asn	Trp	Arg
		442			451			460			469			478				487
	GAA	TTC	AGT	TTT	ATT	CAG	TCT	ACA	CTT	GGA	TAT	GTC	GCT	CTG	CTC	ATA	AGT	ACT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Glu	Phe	Ser	Phe	Ile	Gln	Ser	Thr	Leu	Gly	Tyr	Val	Ala	Leu	Leu	Ile	Ser	Thr
		496			505													

FIG. 10

STEAP-2, AA508880 (NCI_CGAP Pr6) SEQ ID NO:9

ggtcgacttttccctttattcctttgtcagagatctgattcatccatattgctagaaaccaacagagtgacttttaca
aaattcctatagagattgtgaataaaaccttacctatagttgccattactttgtctctccctagtataacctgacgg
tcttctggcagctgcttatcaactttattacggcaccaagtataggagatttccaccttgggtggaaacctggta
cagtgtagaaaacagcttggattactaagttgtttcttcgctatgggtccatgttgccctacagcctctgcttaccga
tgagaagggtcagagagat

STEAP-2, 98P4B6 SSH fragment SEQ ID NO:10

TTTGCAGCTTTGCAGATACCCAGACTGAGCTGGAATTTGTCTTCCTATTGACTCTACTTCTTTAAAGCG
GCTGCCCATTAATTCTCAGCTGTCCTTGCAAGTTAGGTGTACATGTGACTGAGTGTGGCCAGTGAGATGAAGTC
TCCTCAAAGGAAGGCAGCATGTGTCCTTTT

A1139607 (testis EST) SEQ ID NO:11

aagaaggagaatccatttagcacctcctcagcctggctcagtgattcatatgtggctttgggaataacttgggtttt
ttctgtttgtactcttgggaatcacttctttgccatctgttagcaatgcagtcactggagagagtccgatattgt
ccagtcctaaactgggttatttgacctgatcttgtgtacagcccacacctgggtgtacggtgggaagagattcctc
agcccttcaaatctcagatgggtatcttctcgcagcctacgtgttagggcttatcattccttgcaactgtgctgggtga
tcaagtttgcctaatacatgccatgtgttagacaacaccttacaaggatccgccagggtgggaagggaactcaaa
acactagaaaaagcatggaatggaaaaatcaatatataaaacaaagttcaatttagctggaaaaaaaaa

R80991 (placental EST) SEQ ID NO:12

ggccgcggcancgctacgacctggtcaacctggcagtcgaagcaggtcttggccanacaagagccacctctgggtg
aaggaggaggtctggcggtggagatctacctctccctgggagtgctggccctcggcacgttgctccctgctggcg
tgacctcactgccgtccattgcaaaactcgtcaactggaggaggttcagcttcggttcagtcctcactgggtttgt
ggcctcgtgctgagcacactncacacgctcacctacggctggacccgcgccttcgaggagagccgctacaagttc
tacctnctcccaccttcacgntcacgctgctgggtgcctcggttcggttcacctgggccaagccctgttntac
tgcttgcattcagccgnaga

FIG. 11A

STEAP-1	106	FYKIPILVINKVLPVVSITLLALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFG	
STEAP-2	2	FYKIPIEIVNKTLPPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLG	
		*****	** * * * * * * * * * * * * * * * *
STEAP-1	166	LLSFFFVAVLHAIYSLSPMRRSYRYKLLNWAYQQVQONKEDAWIEHDVWRMEIYVSLGIV	
STEAP-2	62	LLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIM	
		*****	* * * * * * * * * * * * * * * *
STEAP-1	226	GLAILALLAVTSIPSVSDSLTWREPHYIQSKLGIVSLLLGTIHALIFAWNK	PORTION OF SEQ ID NO:2
STEAP-2	122	SLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKR	PORTION OF SEQ ID NO:8
		* * *	* * * * * * * * * * * * * * *

FIG. 11B

	271	285	286	300	301	315	316	330	331	345	346	362
STEAP-1	IIPANKNWIDINQFVM	YLPPTF	LTIAVFLPIV	VLVFKSILFLP	CTIRK	KULKIRH	GEDVTKI	NKTEICSQ	L			
STEAP-2	IYWGKRA	---	---	---	---	---	---	---	---			
STEAP-3	VYGGKRLTSPSKLRW	YLPAA	YVLGLIIPCT	VLVKKFVLIM	PCVDN	TLTRIR	QGWERN	SKH	---			
STEAP-4	TYGHTRAFEESIKYF	YLPPTF	TXLLVPCV	RSSWAKALFK	LP	CIQ	P	---	---			
										173	SEQ ID NO:8	
										128	SEQ ID NO:33	
										128	SEQ ID NO:34	

FIG. 17

